



Partial resistance to clubroot in Arabidopsis is based on changes in the host primary metabolism and targeted cell division and expansion capacity

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Résumé en anglais	<p>To date, studies of the molecular basis of disease resistance mainly focused on qualitative resistance. However, deciphering mechanisms underlying quantitative resistance could lead to insights into the relationship between qualitative and quantitative resistance and guide the utilization of these two types of resistance to produce durably resistant cultivars. A functional genomics approach, using the CATMA whole-genome microarray, was used to detect changes in gene expression associated with partial quantitative resistance in the Arabidopsis thaliana-Plasmodiophora brassicae pathosystem. The time course of transcript abundance during partial clubroot resistance response was monitored at the whole plant level, and direct comparisons between partial resistance and susceptibility responses were made using the same host genotype. An increasingly complex host response was revealed, as was the differential influence of P. brassicae infection on the transcription of Arabidopsis genes according to the isolate used. We observed, at the transcriptomic level, that metabolic diversion by the pathogen was reduced or delayed, classical plant defense responses were induced earlier and/or more strongly, and cell enlargement and proliferation were actively inhibited in the partial quantitative resistance response compared to the susceptible one.</p>

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